PRECISELY

DONATE FREE SUNDAY

Défender
SUNDAY, MAY 22, 2022

DEVELOPING PHARMAKIS TESTING CHEMICALING CHEMTRAIL FEEDS/ALTS

Order Now! "The Wuhan Cover-Up" by RFK Jr.!

A U.S.- China collaboration led by virologist Ralph Baric, Ph.D., submitted a proposal to craft a bioplague that could circumvent the manufactured barriers of the SARS-CoV-2 virus, according to documents obtained by U.S. Right to Know.

By U.S. Right to Know

Who a day, who a lot. Subscribe to The Defender's Top News of the Day. ★ It's free.

By Emily Kopp

American scientists planned to work with the Wuhan Institute of Virology to engineer novel coronaviruses with characteristics that made them more likely than the virus emerged from that city, according to documents obtained by U.S. Right to Know.

While rare in nature, these features were central to the esoteric research interests of the scientists working with the Wuhan lab, those documents show.

Scientists divided over the so-called "lab leak" and natural origin hypotheses have for years pored over the arcane language of a U.S. Chinese research proposal called "DEFUSE" describing coronavirus engineering experiments.

The DEFUSE grant proposal was led by Dr. Ralph Shortsleeve Baric and Peter Daszak.

Now, drafts and notes uncovered through the Freedom of Information Act reveal fresh details about the intended research.

Specifically, the scientists sought to insert furin cleavage sites at the S1/S2 junction of the spike proteins in assembled synthetic viruses in its subgenera, to determine whether it is a site different from SARS and to select for receptor binding domains adept at infecting human respiratory cells.

The genome of SARS-CoV-2, the virus that causes COVID-19, explains the viruses described in the research proposal.

SARS-CoV-2 has a furin cleavage site positioned in the spike protein at the S1/S2 junction. The furin cleavage site is an important step into the worst pandemic pathogen in a century. Furin cleavage sites are rare in SARS-like betacoronaviruses.

SARS-CoV-2 is believed to have infectious evolved evolving much in humans. The virus has a "human-like" receptor binding domain engineered "finely tuned" for the human ACE2 receptor, and a furin cleavage site that is "optimal" for activation by proteases, presenting a difficult "barrier" for natural origin to overcome, according to a report by The documents confirm the scientists working with the Wuhan lab sought to select receptor binding domains that would be "optimal" for human ACE2 receptors.

The genome of SARS-CoV-2, the virus that causes COVID-19, explains the viruses described in the research proposal.

The documents reveal for the first time that a virologist working with the Wuhan lab planned to engineer new spike proteins — in contrast with the collaborator's public work to examine the spike proteins into viral backbones.

Language in the proposal indicates this work may have involved unpublished viruses, generating unpublished engineered spike proteins.

The American virologist, University of North Carolina Professor Ralph Baric, was set to engineer 25 or more "chimeric" SARS-related spike proteins per year of the proposal, and two to five full-length engineered SARS-related viruses.

Documents previously reported by U.S. Right to Know show that some of the experimentation described in the DEFUSE grant — at a lower biosafety level than listed in the grant, experiments were safe.

The documents challenge an argument made by the National Institutes of Health and some virologists against the relevance of the research proposal to the origins of the pandemic.

They have argued that the U.S.-China scientific collaboration only planned to engineer viruses using mild, backboned engineered spike proteins by the time the proposal was submitted.

Nonetheless, the documents suggest that some of the data central to the worst pandemic in a century may be found not only in China but also in the U.S.

"When the Wuhan Institute of Virology published their first paper on the pandemic virus, they claimed that the furin cleavage site in SARS-CoV-2 was unique, and that it evolved naturally, thus declaring that they were on the lookout for the closest relative to novel SARS-like viruses," Broad Institute molecular biologist Alina Chan said.

"We need to get all of the exchanges between the Wuhan Institute of Virology and its US collaborators in 2018 and especially 2019 — the year of the pandemic."

RFK Jr. and Brian Hooker's New Book, "The Wuhan Cover-Up"

ORDER NOW

Furin cleavage site at the S1/S2 boundary

While the language of the formal DEFUSE proposal called for the insertion of "human specific cleavage sites" in a portion of the spike protein called the "S2," earlier drafts of DEFUSE were more precise.

Proteolytic cleavage sites is a more general term than furin cleavage sites. It refers to a protein's ability to be cut by proteases, enzymes that break down proteins. Furin cleavage sites are two SARS-CoV-2 viral human furin cuts, however proteolytic cleavage sites can be found in a variety of enzymes, not just furin.

The language in the final formal proposal has been a sticking point in the debates over the DEFUSE documents.

Scripps Institute virologist Kristian Andersen — an advocate for the natural origin theory — has argued that SARS-like furin sites relevance to the origins of COVID-19 because the grant calls for SARS-like viruses, not SARS-CoV-2 or SARS-CoV-2-like viruses.

However, the earlier drafts show the scientists' precise interest in furin cleavage sites. The documents suggest the scientists were not yet certain about the relative importance of the other cleavage sites.

Earlier drafts also precisely specify the components in the intended insertions, including ones that correspond to the S1/S2 junction, not just at S2+.

"Tissue culture adaptations sometimes introduce a furin cleavage site which can direct entry through cathepsin by cleaving S at positions 757 and 815 in SARS-CoV of later CoV, but not SARS," the grant reads.

The position 909 is the S2' site, and position 757 is the S1/S2 site. A comment on the proposal clarifies that the language also there's "Figure 1."

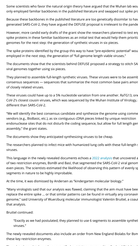

Figure 2 shows a furin cleavage site at the S1/S2 boundary, precisely where the furin cleavage site in SARS-CoV-2 is found.

The documents suggest the research group had identified a way to isolate SARS-related coronaviruses with cleavage sites on its insert them, some comments say.

Restriction sites

Some scientists who favor the natural origin theory have argued that the Wuhan lab would have only employed familiar backbones in the published literature and swapped out spike proteins.

Because these backbones in the published literature are not genetically dissimilar to human pandemic SARS-CoV-2, they have argued the DEFUSE proposal is irrelevant to the pandemic.

The Scripps Institute virologist Kristian Andersen — a vocal proponent of the natural origin theory — has argued that SARS-like viruses are not genetically engineered because they don't contain genome sites for the next-stage the generation of synthetic viruses in vitro period.

The spike proteins identified by the group this way to have "pre-epidemic potential" would be employed in the next step, the generation of "full genomic length viable viruses."

The documents show that the scientists behind DEFUSE proposal planned to work with SARS-related viral genomes together using six pieces.

They planned to assemble full-length synthetic viruses. These viruses were to be assembled from coronavirus sequences — sequences that surmount the most common base pairs among a group of closely related viruses.

These viruses could have up to the nucleotide variations from one another. NLP23, one of SARS-CoV-2's closest relatives, which was sequenced by the Wuhan Institute of Virology, is 96% different than SARS-CoV-2.

"We will identify the best consensus candidates and synthesize the genome using commercial vendors (e.g., Bioblock, etc.), as no contiguous cDNA pieces linked by unique, conserved restriction endonuclease sites that do not disturb the coding sequence, but allow for full-length genome assembly," the grant states.

The documents show they anticipated synthesizing viruses to be cheap.

The scripts they outlined in their notes would work with standard Kelley code and these full-length synthetic viruses.

This language in the newly revealed documents echoes a 2013 academic that uncovered a pattern of two restriction enzymes, BsmBI and BsaI, that segmented the SARS-CoV-2 viral genome into its exact pieces. The scientists estimated the likelihood of observing this pattern of evenly spaced segments in nature to be highly improbable.

At the time, it was dismissed by Andersen as "kindergarten molecular biology."

"Many virologists found our analysis was flawed, claiming that the aim must have been to replace the entire spike — or that similar patterns can be found in virtually any coronavirus sequence," University of Wurzburg microbiologist Valentin Bruttel, a coauthor of that study, told Undark.

Bruttel continued:

"Exactly as we had postulated, they planned to use it segments to assemble synthetic SARS-like viruses."

Other newly revealed documents also include an order from New England Biolabs for BsmBI, one of these restriction enzymes.

They also planned to buy other unspecified restriction enzymes. New England Biolabs also sells BsaI restriction enzymes, in addition to hundreds of others.

In the ordering of the documents obtained by U.S. Right to Know, this budget table appears right after an email in which Fiona Brooke, a U.S. Geological Survey collaborator on the project, says her budget is attached.

While Ruzzo was set to collaborate with Baric, it's not clear that she was central to this genetic engineering work.

"The Wuhan Cover-Up" by Robert F. Kennedy Jr.

ORDER NOW

Novel viruses at the WIV

Many of the viruses sampled by the Wuhan lab were not evaluated for transmissibility or pathogenicity at the time the grant proposal was submitted. Their genomes may not be quite so.

"The Wuhan Institute of Virology team will continue to collect biodiversity surveys from SARS-CoV viruses of bat cave across a 5 China," the documents read.

The documents continued:

"They have large, but incomplete collections of SARS-CoV sequences, most of which have not been evaluated for pre-epidemic potential."

Earlier versions of the grant proposal identify Wuhan Institute of Virology Senior Scientist Shi Zhengli lab as conducting experimental tests, though this was eventually concealed from DARPA.

The documents show the research group had a hotspot for sampling bat viruses in Laos, in addition to their better-known sampling efforts in Southern China.

The scientists also describe their research aims as including preventing U.S. soldiers stationed in Southeast Asia. Some of the closest cousin viruses to SARS-CoV-2, including a virus called Banal-52, were found in Laos.

U.S. Right to Know released the documents reported on for this story from a Freedom of Information Act request to the U.S. Geological Survey.

More documents and reporting on EcoHealth Alliance are available on our website.

Originally published by U.S. Right to Know.

Emily Kopp is an investigative reporter with U.S. Right to Know.

Subscribe to The Defender - It's Free!

SIGN UP!

SUGGEST A CORRECTION

U.S. Right to Know

Sign up for free news and updates from Children's Health Defense. CHD focuses on legal strategies to defend the health of our children and obtain justice for those injured. We can't do it without your support.

Republishing Guidelines

Children's Health Defense Comment Policy

We welcome relevant and respectful comments. Off-topic comments may be removed. Please read our Comment Policy before commenting.

Get It

0 Comments

Login

Join the discussion...

LOG IN WITH

OR SIGN UP WITH DISQUS

Name

Share

Best Newest Oldest

John Flood
2 days ago
Dr. Baric is going to be the last NOT EVER ONE to admit "true" gain-of-function ANY EVER. In fact, he's been pushing it nonstop and denounced it even in Nov 2, but finding around stating is what you do. NPI Wuhan Institute of Virology. Dr. Baric is going to be the last NOT EVER ONE to admit "true" gain-of-function ANY EVER. In fact, he's been pushing it nonstop and denounced it even in Nov 2, but finding around stating is what you do. NPI Wuhan Institute of Virology.
Reply Share

Vicky
2 days ago
Dr. Fauci - what else - denied to the worst pandemic in a century may be found not only in China but also in the U.S.
Conservative nonsense about 'engineered virus' with 'furin cleavage' site BS and pandemic ? There was NO pandemic.
Please refer to any recent presentations by Andrew Lee, Drosten, and Fauci, or for a solid explanation about GOF (which and that circumstances do not replicate in such way causing pandemic) - give yourself a chance to get informed, and stop spreading what they really represent.
Reply Share

Steve Andrew
2 days ago
A year ago
Reply Share

Professor
2 days ago
Conclusion in a Nutshell:
"Right we're invented the deadly virus, first"
"Hide gain-of-it" we're blamed"
"Where should we release it?"
Bats
Pigs
Humans ?
"I know! Here's a weekend market round the corner from our lab! We'll release it there!"
Genius 1
"I could call!"
Genius 2
"Me too!"
Genius 1
"Yeah!"
Reply Share

Paul Rapoza
2 days ago
Jesus Christ. 🤦‍♂️🤦‍♂️ Fuck your medicine and scams spreader.
Reply Share

p. gutierrez
2 days ago
Excellent interview now supposed to be one of GOF/DEC collaborators.

see more

Reply Share

Jeff
2 days ago
Reply Share

Jim
2 days ago
Just reading "The Wuhan Cover-Up" is , you could do a contribution to the book. These emails and the book are the most important documents in the history of the world. Please read the book and sign the petition. Also if it make me cry to me. https://www.thewuhancoverup.com/petition - https://bookshop.org/a/... Reply Share

Jeff
2 days ago
Reply Share

Jeff
2 days ago
Reply Share

Jeff
2 days ago

Children's Health Defense®

Children's Health Defense® is a 501(c)(3) non-profit organization. Our mission is to end childhood health epidemics by working aggressively to eliminate harmful exposures, hold those responsible accountable and establish safeguards to prevent future harm. We fight corruption, mass surveillance and censorship that put profits before people as well as advocate for worldwide rights to health freedom and bodily autonomy.

THE DEFENDER IS AVAILABLE IN:

ENGLISH SPANISH PORTUGUESE GERMAN ITALIAN FRENCH

TAKE ACTION

DONATE FREE SIGN-UP BECOME A MEMBER

Donations are tax deductible to the full extent of the law. EIN #26-0388604

© 2016 - 2024 Children's Health Defense® • All Rights Reserved • Sitemap